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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2518.26 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-8
Perfect score: 1017
Sequence: 1 atgaagttcaccgttgctat.....caggttgcgaaagaaagtaa 1017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	251.6	24.7	840	3	AB045172	AB045172 Reticulit
2	246.8	24.3	828	3	AB045179	AB045179 Reticulit
3	244.2	24.0	780	3	AB045168	AB045168 Reticulit
4	241.8	23.8	808	3	AB045178	AB045178 Reticulit
5	240.6	23.7	710	3	AB045171	AB045171 Reticulit
6	233.4	22.9	774	3	AB045170	AB045170 Reticulit
7	232.8	22.9	781	3	AB045165	AB045165 Reticulit
8	231	22.7	784	3	AB045167	AB045167 Reticulit
9	227.8	22.4	798	3	AB045166	AB045166 Reticulit
10	221.4	21.8	1443	8	FSOKCH	L29381 Fusarium ox
11	221.4	21.8	1473	6	A21795	A21795 F.oxysporum
12	221.4	21.8	1473	6	A23637	A23637 F. oxysporu
13	221.4	21.8	1473	6	A23646	A23646 F. oxysporu
14	221.4	21.8	1473	6	A23955	A23955 Endoglucana
15	221.4	21.8	1473	6	A23959	A23959 Endoglucana
16	221.4	21.8	1473	6	A41660	A41660 Sequence 3
17	221.4	21.8	1473	6	AR072922	AR072922 Sequence
18	221.4	21.8	1473	6	BD002249	BD002249 Cellulase
19	221.4	21.8	1473	6	BD010853	BD010853 Cellulase
20	221.4	21.8	1473	6	I13885	I13885 Sequence 3
21	221.4	21.8	1473	6	I21317	I21317 Sequence 3
22	221.4	21.8	1473	6	I57984	I57984 Sequence 3
23	217.4	21.4	761	3	AB045175	AB045175 Reticulit
24	213.6	21.0	785	3	AB045169	AB045169 Reticulit
25	212.2	20.9	759	3	AB045174	AB045174 Reticulit
26	212.2	20.9	802	3	AB045176	AB045176 Reticulit
27	211.8	20.8	783	3	AB045173	AB045173 Reticulit
28	210.6	20.7	785	3	AB045177	AB045177 Reticulit
29	207.4	20.4	1423	6	AR094309	AR094309 Sequence
30	204	20.1	912	6	A68076	A68076 Sequence 71
31	204	20.1	912	6	AR163170	AR163170 Sequence
32	202.8	19.9	919	6	A68072	A68072 Sequence 67
33	202.8	19.9	919	6	AR163168	AR163168 Sequence
34	200.6	19.7	924	6	A68074	A68074 Sequence 69
35	200.6	19.7	924	6	AR163169	AR163169 Sequence
36	188	18.5	922	6	A68078	A68078 Sequence 73
37	188	18.5	922	6	AR163171	AR163171 Sequence
38	186.8	18.4	922	6	A68070	A68070 Sequence 65
39	186.8	18.4	922	6	AR163167	AR163167 Sequence
40	186	18.3	1154	6	AR094308	AR094308 Sequence
41	184	18.1	1174	6	A92311	A92311 Sequence 1
42	184	18.1	1174	6	AR075389	AR075389 Sequence
43	184	18.1	1174	6	AR094310	AR094310 Sequence
44	179.4	17.6	1057	6	BD002248	BD002248 Cellulase
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ALIGNMENTS

RESULT 1
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LOCUS AB045172 840 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase homologue, clone:8-44, complete cds.
ACCESSION AB045172
VERSION AB045172.1 GI:8926976
KEYWORDS .
SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:8-44.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family

45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
JOURNAL Extremophiles 4 (6), 343-349 (2000)
MEDLINE 21020023
REFERENCE 2 (bases 1 to 840)
AUTHORS Ohkuma,M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

FEATURES Location/Qualifiers
source 1. .840
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BASE COUNT 227 a 157 c 200 g 256 t
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Query Match 24.7%; Score 251.6; DB 3; Length 840;
Best Local Similarity 65.4%; Pred. No. 1.2e-56;
Matches 403; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

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Db        138 TGCTGTGACTCAGCCTGTTGACACATGCGCAAAAGATGGCACAACCAGAGTTGCAAGCAA 197
Qy        522 TGCCAATGCTCAAAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAACAACCAACC 581
Db        198 TGACACAGTGAAATCTTGCTGTGATGGTGGAGAGGGATACATGTGTTATGATCAAGCACC 257
Qy        582 TTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGCTCCAA 641
Db        258 TTGGGCTGTTAATGACTCGGTTGCATACGGTTTTGCCGCTGCAGCTTGCTGTGG---AGG 314
Qy        642 CGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCTTCTGG 701
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Qy        882 TCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACTCTGA 941
Db        555 GCTTCCATCAGGTCTTCAGGCTGGATGCCAGTGGACATTTGATTGGTTCCAAAATGCTGA 614
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Db        615 CAACCCTTCAATCAATTTCAATCAAGTGACCTGCCCAAGTGAATTGACAGCAAAAACCAA 674
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RESULT 2
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LOCUS AB045179 828 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase homologue, clone:6-47, complete cds.
ACCESSION AB045179
VERSION AB045179.1 GI:8926990
KEYWORDS .
SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:6-47.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
JOURNAL Extremophiles 4 (6), 343-349 (2000)
MEDLINE 21020023
REFERENCE 2 (bases 1 to 828)
AUTHORS Ohkuma,M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

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BASE COUNT 231 a 133 c 208 g 256 t
ORIGIN

Query Match 24.3%; Score 246.8; DB 3; Length 828;
Best Local Similarity 64.9%; Pred. No. 2.3e-55;
Matches 400; Conservative 0; Mismatches 207; Indels 9; Gaps 2;

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Db        259 ATGGGCTGTTAATGACTCAGTTGCCTATGGTTTTGCAGCTGCAGCTTGCTGTGG---AGG 315
Qy        642 CGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCTTCTGG 701
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Db        316 TGAGACTGGAGCTTGTTGCAATTGCTATGAGCTTACGTTCACGAGTGGCCCAGTGAATGG 375

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Db        376 AAAGAAGATGGTTGTTCAAGTTACGAACACTGGTGGTGATCTTGGTTCAAACCAATTTGA 435

Qy        762 TTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGGGGCGC 821
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Qy        882 TCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACTCTGA 941
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Qy       1002 TTGCGAAAGAAAGTAA 1017
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RESULT 3
AB045168
LOCUS       AB045168                780 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:4-44, complete cds.
ACCESSION   AB045168
VERSION     AB045168.1  GI:8926968
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:4-44.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 780)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
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  Matches  401;  Conservative    0;  Mismatches  213;  Indels    9;  Gaps    2;

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Qy        520 GATGCCAATGCTC------AAAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAAC 573
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Db        184 GCAAGCAACGATACAGTAAAATCTGGTTGTGATGGCGGTGACGGCTTCATGTGCTACGAT 243

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Qy        634 GGCTCCAACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCT 693
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Db        304 GGAGGTGAGAAGGCTGCCTGCTGTAAT---TGTTACGAGTTGACTTTCACCTCTGGCCCC 360

Qy        694 GCTTCTGGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAAC 753
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Db        361 GTTAATGGCAAGAAGATGACTGTTCAGGTTACCAACACCGGAGGTGATCTCGGTTCGAAT 420

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Qy        994 CGCTCAGGTTGCGAAAGAAAGTA 1016
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Db        661 AAAACCAATTGCAGACGCAATTA 683


RESULT 4
AB045178
LOCUS       AB045178                808 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:45-6, complete cds.
ACCESSION   AB045178
VERSION     AB045178.1  GI:8926988
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:45-6.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 808)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
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           Fax:66-48-462-4672)
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  Best Local Similarity   64.4%;  Pred. No. 5e-54;
  Matches  395;  Conservative    0;  Mismatches  212;  Indels    6;  Gaps    2;

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Qy        468 TTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTAGATGCCAA 527
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Db        141 TTCCGTGTCCAAGCCCGTTGACACATGTGCAAAAGATGGAACAACTCGAGTTGCAACCAG 200

Qy        528 TGCTCAAAGTGGTTG---TAACGGTGGTAATGGTTTCATGTGTAACAACAACCAACCTTG 584
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Db        201 CGCAAAATCAGCTTGCGATAGTGGCGGCACAGCATATATGTGTTATGATCAAACACCGCG 260

Qy        585 GGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGCTCCAACGA 644
              ||||||||||||       ||    || || ||||||||  || || | ||      | |
Db        261 TGCTGTCAATGATTCATATGCCATTGGGTTTGCTGCTGCGGCTGTTTCAGGTGGTGAGAA 320

Qy        645 AGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCTTCTGGAAA 704
              ||| |   ||| |||   ||||| ||| | || |||||||||||| ||| |  ||||||
Db        321 AGCGG---CGTGCTGTACGTGTTACGAACTCACTTTCACTTCTGGCCCTGTTAATGGAAA 377

Qy        705 GAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCACTTTGATTT 764
              |||||||  |||||||| ||||| || || || ||| | || || || || |||||| |
Db        378 GAAGATGACTGTTCAAGTGACCAATACGGGAGGTGATCTTGGTTCCAATCAATTTGATAT 437

Qy        765 GCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGGGGCGCTCC 824
              || ||||| || || ||||| | | ||| || ||  || |||||| ||| || ||
Db        438 TGCGATTCCCGGCGGAGGTGTTGGACTTTACAACGGTTGCACTTCTCAATCGGGTGCACC 497

Qy        825 CAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTGTGCCTCTCT 884
              |||||  ||||||    |||||||  |||||   ||||     ||| ||| |    ||
Db        498 TGCAGATGGATGGGGAAGCCGATATGGAGGTGTTTCCTCTCGAAGTGAGTGTTCTCAGCT 557

Qy        885 TCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACTCTGATAA 944
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Db        558 TCCTTCTGGTCTTCAAGCCGGGTGCCAGTGGCGTTTTGACTGGTTCCAAAATGCTGATAA 617

Qy        945 CCCTACCATGACCTTCAAGGAAGTTACCTGTCCTGCTGAATTAACTACTCGCTCAGGTTG 1004
              ||  | || || ||||| ||||| |  ||||| | ||| || || |      |    |||
Db        618 TCCGTCAATTACATTCAACGAAGTGAGTTGTCCAGGTGACTTGACAAGCAAAACCAATTG 677

Qy       1005 CGAAAGAAAGTAA 1017
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Db        678 CAGACGCCAGTAA 690


RESULT 5
AB045171
LOCUS       AB045171                 710 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:7-50, complete cds.
ACCESSION   AB045171
VERSION     AB045171.1  GI:8926974
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:7-50.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 710)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Reticulitermes speratus hindgut symbiont
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                     /clone="7-50"
     CDS             20. .679
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BASE COUNT      185 a    137 c    197 g    191 t
ORIGIN

  Query Match           23.7%;  Score 240.6;  DB 3;  Length 710;
  Best Local Similarity   64.1%;  Pred. No. 1e-53;
  Matches  398;  Conservative    0;  Mismatches  214;  Indels    9;  Gaps    2;

Qy        403 GGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCTGGA 462
              | ||| ||    ||||| |||||||||||||||| |||||    ||   |||    |
Db         62 GACAGCGGAAGAACAACCCGTTATTGGGATTGTTGCAAAGCCAGCTGTGCGTGGGAAAAA 121

Qy        463 AAAGCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTAG-- 520
              ||||||  |||| ||    |||||||||||| ||||       |||| | | |   | | |
Db        122 AAAGCTGCTGTTACACAGCCTGTTGACACTTGTGGAAAAGATGGGACCACGAGAGTTGCG 181

Qy        521 ----ATGCCAATGCTCAAAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAACAAC 576
                  ||| || ||   ||   | |||| | ||||| | || |  |||||| |  | |
Db        182 AGCAATGACACTGTGAAATCAGCTTGTGATGGTGGAGAAGGATATATGTGTTATGATCAA 241

Qy        577 CAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGC 636
                ||| ||||| || |||||      | || |||||||| ||||||||  ||     |||
Db        242 GCACCATGGGCAGTTAATGACTCTGTTGCGTACGGTTTTGCTGCTGCAGCTTGCTGTGG- 300

Qy        637 TCCAACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCT 696
                  ||||  |||   || ||   || |||||  | || ||||  |||  | |
Db        301 --GGGCGAAAGCGGAGCTTGCTGCAATTGCTATGAGCTTACATTCACAAGTGGACCAGTG 358

Qy        697 TCTGGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCAC 756
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Db        359 AATGGAAAGAAGATGGTTGTACAAGTCACCAACACCGGTGGTGATCTTGGCTCGAATCAG 418

Qy        757 TTTGATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGG 816
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Db        419 TTTGATCTTGCGATTCCGGGTGGAGGTGTTGGGATCTACAACGGTTGCACCCAGCAATCA 478

Qy        817 GGCGCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTGT 876
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Db        479 GGTGCACCTGCTGATGGATGGGGAAGCCGATATGGAGGTGTTTCATCCCGCAGCGAATGC 538

Qy        877 GCCTCTCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAAC 936

Db        539 TCTCAGCTTCCGTCGGGCCTTCAAGCTGGGTGCCAATGGAGATTTGATTGGTTCCAAAAT 598

Qy        937 TCTGATAACCCTACCATGACCTTCAAGGAAGTTACCTGTCCTGCTGAATTAACTACTCGC 996

Db        599 GCCGATAACCCTTCAATCAATTTCAACCAAGTGACATGCCCTGGTGAGTTAACGGCAAAA 658

Qy        997 TCAGGTTGCGAAAGAAAGTAA 1017

Db        659 ACCAATTGCAAGCGCACTTAA 679


RESULT 6
AB045170
LOCUS       AB045170                774 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:8-38, complete cds.
ACCESSION   AB045170
VERSION     AB045170.1  GI:8926972
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:8-38.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 774)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
FEATURES             Location/Qualifiers
     source          1. .774
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     CDS             52. .714
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BASE COUNT      179 a    144 c    212 g    239 t
ORIGIN

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Db        100 ACTGGCAGAACAACCCGTTATTGGGATTGCTGCAAAGGAAGTTGTGGCTGGGAGAAGAAG 159

Qy        466 GCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTAG----- 520

Db        160 GCTAATGTGGACAAGCCTATTGATACGTGCGCAAAAGATGGTACCACCAGAGTTGCAAGC 219

Qy        521 -ATGCCAATGCTCAAAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAACAACCAA 579

Db        220 AACGACACCGTTAAGTCAGGCTGTGATGGCGGAGATGGATATATGTGTTATGATCAATCT 279

Qy        580 CCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGCTCC 639

Db        280 CCGTGGGGTGTCAATGATTCTTTTGCTCTGGGTTTTGCTGCTGCAGCGGTTTCAGGAGGT 339

Qy        640 AACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCTTCT 699

Db        340 GAGAGCGCTGCCTGCTGCAAT---TGTTACGAGTTAACATTCACTTCTGGCCCAGTTAAT 396

Qy        700 GGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCACTTT 759

Db        397 GGAAAGAAGATGACTGTTCAGGTTACCAACACTGGGGGTGACCTTGGTTCCAATCAGTTT 456

Qy        760 GATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGGGGC 819

Db        457 GATCTTGCCATTCCAGGTGGTGGTGTTGGAATCTACAACGGCTGTACCGCTCAATCTGGT 516

Qy        820 GCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTGTGCC 879

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Qy        880 TCTCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAACTCT 939

Db        577 CAGCTTCCGTCGGGACTTCAGGCTGGCTGCCAGTGGCGTTTTGACTGGTTCCAGAACGCT 636

Qy        940 GATAACCCTACCATGACCTTCAAGGAAGTTACCTGTCCTGCTGAATTAACTAC 992

Db        637 GATAATCCGTCAATCAGCTTCAACGTGGTTTCGTGTCCTAGTGAGTTGATTGC 689


RESULT 7
AB045165
LOCUS       AB045165                781 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:2-54, complete cds.
ACCESSION   AB045165
VERSION     AB045165.1  GI:8926962
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:2-54.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 781)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
FEATURES             Location/Qualifiers
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RN"
BASE COUNT 193 a 143 c 210 g 235 t
ORIGIN

Query Match 22.9%; Score 232.8; DB 3; Length 781;
Best Local Similarity 63.4%; Pred. No. 1.3e-51;
Matches 392; Conservative 0; Mismatches 217; Indels 9; Gaps 2;

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Qy        406 AGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCTGGAAAA 465
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Db         73 AGTGGCAGAACAACCCGGTACTGGGATTGCTGCAAAGGAAGTTGTGGGTGGGAAGCAAAG 132

Qy        466 GCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTAG----- 520
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Db        133 GCTGATGTAAGCAAGCCTATTGATACATGTGCGAAAGATGGCACAACAAGAGTTGCAAGT 192

Qy        521 -ATGCCAATGCTCAAAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAACAACCAA 579
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Db        193 AACGATACGGTTAAATCCGGCTGTGATGGTGGAGAAGGATACATGTGTTATGATCAAACG 252

Qy        580 CCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGCTCC 639
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Db        253 CCTCGTGCTGTCAATGATTCTTATGCCATTGGCTTCGCCGCTGCGGCTATCTCAGGAGGA 312

Qy        640 AACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCTTCT 699
               |  | ||||     |||||    ||||| |||||||| ||||| || ||  | |    |
Db        313 GAGAAGGCTG---CTTGTTGCCAGTGTTACGAATTGACTTTCACCTCGGGACCGGTGAAT 369

Qy        700 GGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCACTTT 759
              ||||||||||||  ||||||||||| ||||| || |||||| | || || ||| |||| |||
Db        370 GGAAAGAAGATGACTGTTCAAGTTACTAACACTGGGGGCGATCTTGGTTCCAACCAGTTT 429

Qy        760 GATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGGGGC 819
              |||  |    || || || ||||| || || || |  ||||| ||  |  |||||||  ||
Db        430 GATCTTGCTATTCCAGGGGGTGGTGTGGGAATATATAATGGATGCACCGCTCAATCTGGT 489

Qy        820 GCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTGTGCC 879
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Db        490 GCTCCTGCAGATGGATGGGGAAGCCGATATGGCGGTGTTTCCTCTCGTAGTGAATGTTCC 549

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Db        550 CAGCTTCCATCAGGTCTTCAGGCTGGATGCCAGTGGCGATTTGATTGGTTCCAAAATGCA 609

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Db        610 GATAATCCGTCCATCAACTTCAACGTCGTATCGTGCCCTGGTGAACTGATTGCCAACACC 669

Qy       1000 GGTTGCGAAAGAAAGTAA 1017
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Db        670 AATTGCAGACGTAATTAA 687
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RESULT 8
AB045167
LOCUS AB045167 784 bp mRNA linear INV 14-FEB-2001
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45 cellulase, homologue, clone:8-16, complete cds.
ACCESSION AB045167
VERSION AB045167.1 GI:8926966
KEYWORDS .
SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:8-16.
ORGANISM Reticulitermes speratus hindgut symbiont 130484
Unclassified.
REFERENCE 1 (sites)
AUTHORS Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
JOURNAL Extremophiles 4 (6), 343-349 (2000)
MEDLINE 21020023

REFERENCE 2 (bases 1 to 784)
AUTHORS Ohkuma,M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan
(E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
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/clone="8-16"
CDS 28..690
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RN"
BASE COUNT 202 a 153 c 210 g 219 t
ORIGIN

Query Match 22.7%; Score 231; DB 3; Length 784;
Best Local Similarity 63.1%; Pred. No. 4e-51;
Matches 392; Conservative 0; Mismatches 220; Indels 9; Gaps 2;

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Qy        402 TGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCTGG 461
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Qy        462 AAAAGCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTAG- 520
              ||| ||   ||| |      ||  ||||||| || ||      |||| | | |   | | |
Db        132 AAAGGCCGATGTTAGCAAGCCCATTGACACATGCGCGAAAGATGGGACCACCAGAGTTGC 191

Qy        521 -----ATGCCAATGCTCAAAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAACAA 575
                   | | ||  |  ||||||||||| | || ||  | || | ||||||  |  | | |
Db        192 AAGCAACGACACCGTGAAAAGTGGTTGTGATGGCGGGGACGGATACATGTGCTATGATCA 251

Qy        576 CCAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGG 635
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Db        252 AACACCGTGGGGTGTTAATGATTCATATGCCCTTGGCTTTGCTGCTGCAGCAATTTCAGG 311

Qy        636 CTCCAACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGC 695
                | |  | || | |   || ||  |||||| ||| | || ||||| |||||| | |
Db        312 AGGCGAAAAGGCCGCA---TGCTGCAAACTGTTACGAACTTACGTTCACCTCTGGCCCCGT 368

Qy        696 TTCTGGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCA 755
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Db        369 CAATGGCAAGAAGATGACTGTGCAGGTTACCAACACTGGAGGCGACTTGGGTTCCAACCA 428

Qy        756 CTTTGATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATG 815
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Db        489 TGGTGCTCCTGCCGATGGGTGGGGAAGTCGGTATGGAGGGGTTTCCTCTCGCAGCGAATG 548

Qy        876 TGCCTCTCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAA 935
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Qy        936 CTCTGATAACCCTACCATGACCTTCAAGGAAGTTACCTGTCCTGCTGAATTAACTACTCG 995
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Db        609 TGCCGACAATCCGTCCATGAACTTCAACGTCGTGTCGTGCCCCAGCGAGTTGATTGCGAA 668

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Db        669 AACCAATTGCAGACGCAATTA 689
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RESULT 9
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LOCUS       AB045166                798 bp    mRNA    linear   INV 14-FEB-2001
DEFINITION  Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
            cellulase homologue, clone:2-6, complete cds.
ACCESSION   AB045166
VERSION     AB045166.1  GI:8926964
KEYWORDS    .
SOURCE      Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
            clone:2-6.
  ORGANISM  Reticulitermes speratus hindgut symbiont 130484
            Unclassified.
REFERENCE   1  (sites)
  AUTHORS   Ohtoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
  TITLE     Diverse genes of cellulase homologues of glycosyl hydrolase family
            45 from the symbiotic protists in the hindgut of the termite
            Reticulitermes speratus
  JOURNAL   Extremophiles 4 (6), 343-349 (2000)
  MEDLINE   21020023
REFERENCE   2  (bases 1 to 798)
  AUTHORS   Ohkuma,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
            Physical and Chemical Research), Microbiology Laboratory; Hirosawa
            2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
            Fax:66-48-462-4672)
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BASE COUNT      195 a    154 c    226 g    222 t      1 others
ORIGIN

  Query Match             22.4%;  Score 227.8;  DB 3;  Length 798;
  Best Local Similarity   62.8%;  Pred. No. 2.9e-50;
  Matches  390;  Conservative    0;  Mismatches  222;  Indels    9;  Gaps    2;

Qy        402 TGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCTGG 461
              || ||||||    |||||  | |||||||| || || || |    |||  |||||   |
Db         74 TGACAGTGGCAAAACAACAAGGTATTGGGACTGCTGCAAGGGCAGTTGTGGCTGGGAAGC 133

Qy        462 AAAAGCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTAG- 520
              |||||    || |    ||  ||||||| || ||     | || | | |   | | |
Db        134 GAAAGCGGACGTGAGCAAGCCCATTGACACATGCGCGAAAGACCGGACCACCAGAGTTGC 193

Qy        521 -----ATGCCAATGCTCAAAGTGGTTGTAACGGTGGTAATGGTTTCATGTGTAACAACAA 575
                  | | ||  |   | |||||||||| | || ||  | ||||  |||||  |  | |
Db        194 GAGCAACGACACCGTGAAGAGTGGTTGTGATGGCGGGGACGGTTATATGTGCTATGATCA 253

Qy        576 CCAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGG 635
              ||| ||||  ||||| ||       |||    || || ||||||||  | ||| | ||
Db        254 AACACCGTGGGGCGTCAACGACTCATACGCCCTGGGCTTTGCTGCTGCAGCAATTTCAGG 313

Qy        636 CTCCAACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGC 695
              | | |  | ||||     || ||   ||||||||||||||| ||||||||||| | |
Db        314 CGGCGAGAAGGCTG---CTTGCTGCAACTGTTATGAATTGACATTCACTTCTGGCCCCGT 370

Qy        696 TTCTGGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCA 755
              |  ||| |||||||||   || || |||||||||| || ||||| || || || || ||
Db        371 TAATGGCAAGAAGATGACAGTACAGGTTACCAACACTGGAGGCGACTTGGGTTCCAATCA 430

Qy        756 CTTTGATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATG 815
              ||||||  |   ||| || || || || || || |||| |||||| ||  | ||||| |
Db        431 ATTTGATCTTGCAATTCCAGGCGGCGGTGTGGGCATCTACAATGGATGCACGGCTCAGTC 490

Qy        816 GGGCGCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTG 875
              ||||||||   ||| || |||||   | | ||||||||  ||   ||||  |   || ||
Db        491 TGGCGCTCCTGCTGACGGATGGGGTAGTCGGTATGGTGGAGTTTCCTCTCGCAGCGAATG 550

Qy        876 TGCCTCTCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAA 935
              |    ||||| || | |||||| ||||| ||  | ||||||||  | ||||||  | ||
Db        551 CTCGCAACTTCCTTCAGGTCTTCAGGCTGGCTGCCAGTGGAGATTTGATTGGTTCCAAAA 610

Qy        936 CTCTGATAACCCTACCATGACCTTCAAGGAAGTTACCTGTCCTGCTGAATTAACTACTCG 995
              | | || || ||  |||||  |||||  |  ||  | || ||  ||| || | | |
Db        611 CGCCGACAATCCGTCCATGAATTTCAATGTGGTGTCGTGCCCCAGTGAGTTGATTGCGAA 670

Qy        996 CTCAGGTTGCGAAAGAAAGTA 1016
              |   ||||  | | || ||
Db        671 AACCAATTGCAGACGCAATTA 691


RESULT 10
FSOKCH
LOCUS       FSOKCH                  1443 bp    mRNA    linear   PLN 28-APR-1995
DEFINITION  Fusarium oxysporum K-family cellulase homologue mRNA, complete cds.
ACCESSION   L29381
VERSION     L29381.1  GI:520822
KEYWORDS    K-family cellulase homologue; cellulase; homologue.
SOURCE      Fusarium oxysporum cDNA to mRNA.
  ORGANISM  Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1  (bases 1 to 1443)
  AUTHORS   Sheppard,P.O., Grant,F.J., Oort,P.J., Sprecher,C.A., Foster,D.C.,
            Hagen,F.S., Upshall,A., McKnight,G.L. and O'Hara,P.J.
  TITLE     The use of conserved cellulase family-specific sequences to clone
            cellulase homologue cDNAs from Fusarium oxysporum
  JOURNAL   Gene 150 (1), 163-167 (1994)
  MEDLINE   95047531
   PUBMED   7959045
FEATURES             Location/Qualifiers
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                     /organism="Fusarium oxysporum"
                     /db_xref="taxon:5507"
     CDS             83. .1213
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                     /codon_start=1
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                     /protein_id="AAA65589.1"
                     /db_xref="GI:520823"
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                     ALGGAQYGGISSRSECDSYPELLKDGCHWRFDWFENADNPDPTFEQVQCPKALLDISG
                     CKRDDDSSFPAFKGDTSASKPQPSSSAKKTTSAAAAAQPQKTKDSAPVVQKSSTKPAA
                     QPEPTKPADKPQTDKPVATKPAATKPAQPVNKPKTTQKVRGTKTRGSCPAKTDATAKA
                     SVVPAYYQCGGSKSAYPNGNLACATGSKCVKQNEYYSQCVPN"
BASE COUNT      325 a    448 c    332 g    338 t
ORIGIN

  Query Match             21.8%;  Score 221.4;  DB 8;  Length 1443;
  Best Local Similarity   63.9%;  Pred. No. 1.7e-48;
  Matches  371;  Conservative    0;  Mismatches  201;  Indels    9;  Gaps    2;

Qy        400 TCTGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCT 459
              ||||| || |||  | | ||||| || |||||||| || ||  ||||||||    |||
Db        137 TCTGGAAGCGGTCACTCTACTCGATACTGGGATTGCTGCAAGCCTTCTTGCTCTTGGAGC 196

Qy        460 GGAAAAGCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTA 519
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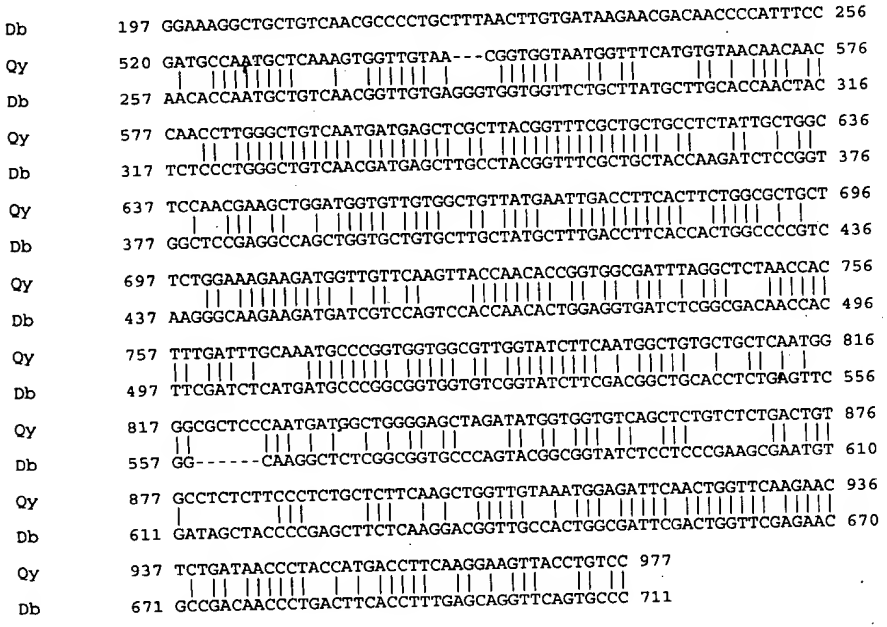

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RESULT 11
A21795
LOCUS       A21795                 1473 bp    mRNA    linear   PAT 20-SEP-1995
DEFINITION  F.oxysporum mRNA for endonuclease component.
ACCESSION   A21795
VERSION     A21795.1  GI:1246874
KEYWORDS    .
SOURCE      Fusarium oxysporum.
  ORGANISM  Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
FEATURES             Location/Qualifiers
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                     /strain="DSM 2672"
                     /db_xref="taxon:5507"
     CDS             97. .1227
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                     ALGGAQYGGISSRSECDSYPELLKDGCHWRFDWFENADNPDFTFEQVQCPKALLDISG
                     CKRDDDSSFPAFKVDTSASKPQPSSSAKKTTSAAAAAQPQKTKDSAPVVQKSSTKPAA
                     QPEPTKPADKPQTDKPVATKPAATKPVQPVNKPKTTQKVRGTKTRGSCPAKTDATAKA
                     SVVPAYYQCGGSKSAYPNGNLACATGSKCVKQNEYYSQCVPN"
BASE COUNT      343 a    453 c    337 g    340 t
ORIGIN

  Query Match           21.8%;  Score 221.4;  DB 6;  Length 1473;
  Best Local Similarity   63.9%;  Pred. No. 1.7e-48;
  Matches  371;  Conservative    0;  Mismatches  201;  Indels    9;  Gaps    2;
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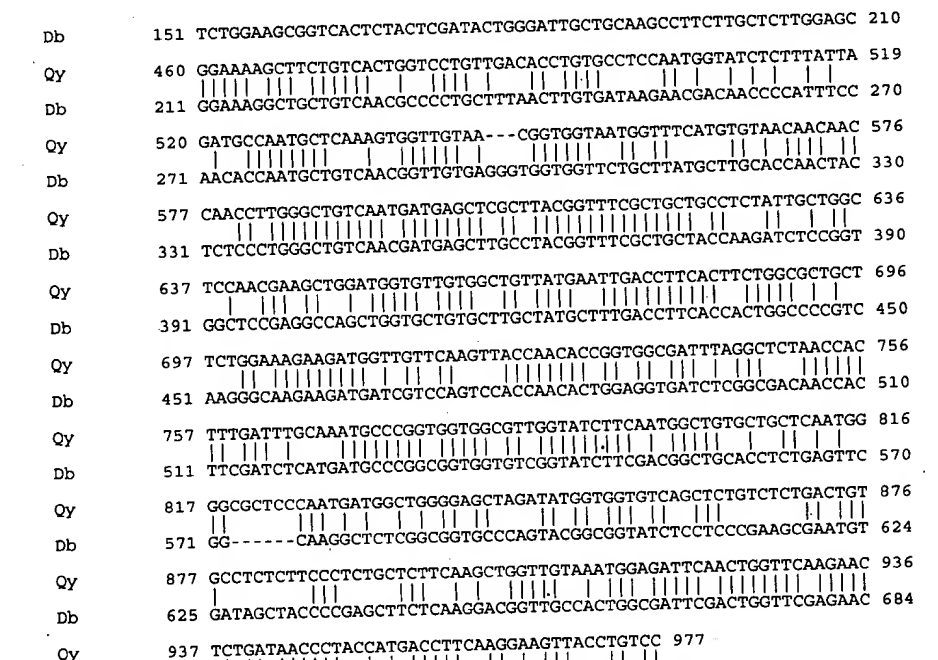

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RESULT 12
A23637
LOCUS       A23637                 1473 bp    mRNA    linear   PAT 19-SEP-1995
DEFINITION  F. oxysporum endoglucanase gene.
ACCESSION   A23637
VERSION     A23637.1  GI:832888
KEYWORDS    endoglucanase.
SOURCE      Fusarium oxysporum.
  ORGANISM  Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1  (bases 1 to 1473)
  AUTHORS   Convents,A.C., Busch,A. and Baeck,A.C.
  TITLE     Detergent compositions with high activity cellulase and softening
            clays
  JOURNAL   Patent: EP 0495258-A 3 22-JUL-1992;
            THE PROCTER & GAMBLE COMPANY
FEATURES             Location/Qualifiers
     source          1. .1473
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     CDS             97. .1227
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                     /protein_id="CAA01682.1"
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BASE COUNT      343 a    453 c    337 g    340 t
ORIGIN

  Query Match           21.8%;  Score 221.4;  DB 6;  Length 1473;
  Best Local Similarity   63.9%;  Pred. No. 1.7e-48;
  Matches  371;  Conservative    0;  Mismatches  201;  Indels    9;  Gaps    2;

Qy        400 TCTGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCT 459
              ||||| || |||  | | ||||| || |||||||| || ||  ||||||||   |||
Db        151 TCTGGAAGCGGTCACTCTACTCGATACTGGGATTGCTGCAAGCCTTCTTGCTCTTGGAGC 210

Qy        460 GGAAAAGCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTA 519
              ||||| ||| ||||||  |  |||| |  || ||||     || |  | | |  | |
Db        211 GGAAAGGCTGCTGTCAACGCCCCTGCTTTAACTTGTGATAAGAACGACAACCCCATTTCC 270

Qy        520 GATGCCAATGCTCAAAGTGGTTGTAA---CGGTGGTAATGGTTTCATGTGTAACAACAAC 576
              |  ||||||||   | ||||||  |    ||||||  || ||     || | |||| ||
Db        271 AACACCAATGCTGTCAACGGTTGTGAGGGTGGTGGTTCTGCTTATGCTTGCACCAACTAC 330

Qy        577 CAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGC 636
              || |||||||||| |||||||| || |||||||||||||| ||   ||  | ||
Db        331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGCTGCTACCAAGATCTCCGGT 390

Qy        637 TCCAACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCT 696
              |  ||| ||  | ||||| |||| || |||| ||||||||||  ||||| | |
Db        391 GGCTCCGAGGCCAGCTGGTGCTGTGCTTGCTATGCTTTGACCTTCACCACTGGCCCCGTC 450

Qy        697 TCTGGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCAC 756
              || |||||||| | || ||    |||||||| || || ||| | |||   ||||||
Db        451 AAGGGCAAGAAGATGATCGTCCAGTCCACCAACACTGGAGGTGATCTCGGCGACAACCAC 510

Qy        757 TTTGATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGG 816
              || ||| |    |||||||| ||||| || ||||||||| | |||||  |  || | |
Db        511 TTCGATCTCATGATGCCCGGCGGTGGTGTCGGTATCTTCGACGGCTGCACCTCTGAGTTC 570

Qy        817 GGCGCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTGT 876
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Db        571 GG------CAAGGCTCTCGGCGGTGCCCAGTACGGCGGTATCTCCTCCCGAAGCGAATGT 624

Qy        877 GCCTCTCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAAC 936
              |         |||     ||| | |  ||||| | ||| ||||| ||||||| |||||
Db        625 GATAGCTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTCGACTGGTTCGAGAAC 684

Qy        937 TCTGATAACCCTACCATGACCTTCAAGGAAGTTACCTGTCC 977
              | || ||||||  | | |||||  || | |||   || ||
Db        685 GCCGACAACCCTGACTTCACCTTTGAGCAGGTTCAGTGCCC 725


RESULT 13
A23646
LOCUS       A23646                 1473 bp    mRNA    linear   PAT 23-FEB-1995
DEFINITION  F. oxysporum endoglucanase gene.
ACCESSION   A23646
VERSION     A23646.1  GI:832892
KEYWORDS    .
SOURCE      Fusarium oxysporum.
  ORGANISM  Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1  (bases 1 to 1473)
  AUTHORS   Convents,A.C., Busch,A. and Baeck,A.C.
  TITLE     Detergent compositions with high activity cellulase and quaternary
            ammonium compounds
  JOURNAL   Patent: EP 0495554-A 3 22-JUL-1992;
            THE PROCTER & GAMBLE COMPANY
FEATURES             Location/Qualifiers
     source          1. .1473
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                     /strain="DSM 2672"
                     /db_xref="taxon:5507"
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                     /product="endoglucanase"
                     /protein_id="CAA01684.1"
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                     APALTCDKNDNPISNTNAVNGCEGGGSAYACTNYSPWAVNDELAYGFAATKISGGSEA
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                     ALGGAQYGGISSRSECDSYPELLKDGCHWRFDWFENADNPDFTFEQVQCPKALLDISG
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                     QPEPTKPADKPQTDKPVATKPAATKPVQPVNKPKTTQKVRGTKTRGSCPAKTDATAKA
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BASE COUNT      343 a    453 c    337 g    340 t
ORIGIN

  Query Match           21.8%;  Score 221.4;  DB 6;  Length 1473;
  Best Local Similarity   63.9%;  Pred. No. 1.7e-48;
  Matches  371;  Conservative    0;  Mismatches  201;  Indels    9;  Gaps    2;

Qy        400 TCTGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCT 459
              ||||| || |||  | | ||||| || |||||||| || ||  ||||||||   |||
Db        151 TCTGGAAGCGGTCACTCTACTCGATACTGGGATTGCTGCAAGCCTTCTTGCTCTTGGAGC 210

Qy        460 GGAAAAGCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTA 519
              ||||| ||| ||||||  |  |||| |  || ||||     || |  | | |  | |
Db        211 GGAAAGGCTGCTGTCAACGCCCCTGCTTTAACTTGTGATAAGAACGACAACCCCATTTCC 270

Qy        520 GATGCCAATGCTCAAAGTGGTTGTAA---CGGTGGTAATGGTTTCATGTGTAACAACAAC 576
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Db        271 AACACCAATGCTGTCAACGGTTGTGAGGGTGGTGGTTCTGCTTATGCTTGCACCAACTAC 330

Qy        577 CAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGC 636
              || |||||||||| |||||||| || |||||||||||||| ||   ||  | ||
Db        331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGCTGCTACCAAGATCTCCGGT 390

Qy        637 TCCAACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCT 696
              |  ||| ||  | ||||| |||| || |||| ||||||||||  ||||| | |
Db        391 GGCTCCGAGGCCAGCTGGTGCTGTGCTTGCTATGCTTTGACCTTCACCACTGGCCCCGTC 450

Qy        697 TCTGGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCAC 756
              || |||||||| | || ||    |||||||| || || ||| | |||   ||||||
Db        451 AAGGGCAAGAAGATGATCGTCCAGTCCACCAACACTGGAGGTGATCTCGGCGACAACCAC 510

Qy        757 TTTGATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGG 816
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Db        511 TTCGATCTCATGATGCCCGGCGGTGGTGTCGGTATCTTCGACGGCTGCACCTCTGAGTTC 570

Qy        817 GGCGCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTGT 876
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Db        571 GG------CAAGGCTCTCGGCGGTGCCCAGTACGGCGGTATCTCCTCCCGAAGCGAATGT 624

Qy        877 GCCTCTCTTCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAAC 936
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Db        625 GATAGCTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTCGACTGGTTCGAGAAC 684

Qy        937 TCTGATAACCCTACCATGACCTTCAAGGAAGTTACCTGTCC 977
              | || ||||||  | | |||||  || | |||   || ||
Db        685 GCCGACAACCCTGACTTCACCTTTGAGCAGGTTCAGTGCCC 725


RESULT 14
A23955
LOCUS       A23955                 1473 bp    DNA     linear   PAT 01-MAR-1995
DEFINITION  Endoglucanase gene.
ACCESSION   A23955
VERSION     A23955.1  GI:832896
KEYWORDS    .
SOURCE      Fusarium oxysporum.
  ORGANISM  Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1  (bases 1 to 1473)
  AUTHORS   Baeck,A.C., Busch,A. and Ceulemans,R.A.A.
  TITLE     Compact detergent compositions with high activity cellulase
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  JOURNAL   Patent: EP 0495257-A 3 22-JUL-1992;
            THE PROCTER & GAMBLE COMPANY
FEATURES             Location/Qualifiers
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                     QPEPTKPADKPQTDKPVATKPAATKPVQPVNKPKTTQKVRGTKTRGSCPAKTDATAKA
                     SVVPAYYQCGGSKSAYPNGNLACATGSKCVKQNEYYSQCVPN"
BASE COUNT      343 a    453 c    337 g    340 t
ORIGIN

  Query Match           21.8%;  Score 221.4;  DB 6;  Length 1473;
  Best Local Similarity  63.9%;  Pred. No. 1.7e-48;
  Matches  371;  Conservative    0;  Mismatches  201;  Indels    9;  Gaps    2;

Qy        400 TCTGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCT 459
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Db        151 TCTGGAAGCGGTCACTCTACTCGATACTGGGATTGCTGCAAGCCTTCTTGCTCTTGGAGC 210

Qy        460 GGAAAAGCTTCTGTCACTGGTCCTGTTGACACCTGTGCCTCCAATGGTATCTCTTTATTA 519
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Db        211 GGAAAGGCTGCTGTCAACGCCCCTGCTTTAACTTGTGATAAGAACGACAACCCCATTTCC 270

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Qy        577 CAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGC 636
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Db        331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGCTGCTACCAAGATCTCCGGT 390

Qy        637 TCCAACGAAGCTGGATGGTGTTGTGGCTGTTATGAATTGACCTTCACTTCTGGCGCTGCT 696
              | ||| ||  | ||||| |||| || ||||  ||||||||||  |||||  | |
Db        391 GGCTCCGAGGCCAGCTGGTGCTGTGCTTGCTATGCTTTGACCTTCACCACTGGCCCCGTC 450

Qy        697 TCTGGAAAGAAGATGGTTGTTCAAGTTACCAACACCGGTGGCGATTTAGGCTCTAACCAC 756
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Db        451 AAGGGCAAGAAGATGATCGTCCAGTCCACCAACACTGGAGGTGATCTCGGCGACAACCAC 510

Qy        757 TTTGATTTGCAAATGCCCGGTGGTGGCGTTGGTATCTTCAATGGCTGTGCTGCTCAATGG 816
              || ||| |    |||||||| ||||| || |||||||| | |||||  |  || | |
Db        511 TTCGATCTCATGATGCCCGGCGGTGGTGTCGGTATCTTCGACGGCTGCACCTCTGAGTTC 570

Qy        817 GGCGCTCCCAATGATGGCTGGGGAGCTAGATATGGTGGTGTCAGCTCTGTCTCTGACTGT 876
              ||    ||| | |  | | || ||    || || ||| ||  |||         || |||
Db        571 GG------CAAGGCTCTCGGCGGTGCCCAGTACGGCGGTATCTCCTCCCGAAGCGAATGT 624

Qy        877 GCCTCTCTTCCCCTCTGCTCTTCAAGCTGGTTGTAAATGGAGATTCAACTGGTTCAAGAAC 936
              |       |||    |||  | |  |||||  | ||| ||||| |||||||| |||||
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Qy        937 TCTGATAACCCTACCATGACCTTCAAGGAAGTTACCTGTCC 977
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RESULT 15
A23959
LOCUS       A23959                 1473 bp    DNA     linear   PAT 01-MAR-1995
DEFINITION  Endoglucanase gene.
ACCESSION   A23959
VERSION     A23959.1  GI:832900
KEYWORDS    .
SOURCE      Fusarium oxysporum.
  ORGANISM  Fusarium oxysporum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1  (bases 1 to 1473)
  AUTHORS   McCorquodale,F. and Busch,A.
  TITLE     Dye transfer inhibiting compositions
  JOURNAL   Patent: EP 0540784-A 3 12-MAY-1993;
            THE PROCTER & GAMBLE COMPANY
FEATURES             Location/Qualifiers
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                     /protein_id="CAA01699.1"
                     /db_xref="GI:832901"
                     /translation="MRSYTLLALAGPLAVSAASGSGHSTRYWDCCKPSCSWSGKAAVN
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                     ALGGAQYGGISSRSECDSYPELLKDGCHWRFDWFENADNPDFTFEQVQCPKALLDISG
                     CKRDDDSSFPAFKVDTSASKPQPSSSAKKTTSAAAAAQPQKTKDSAPVVQKSSTKPAA
                     QPEPTKPADKPQTDKPVATKPAATKPVQPVNKPKTTQKVRGTKTRGSCPAKTDATAKA
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BASE COUNT      343 a    453 c    337 g    340 t
ORIGIN

  Query Match           21.8%;  Score 221.4;  DB 6;  Length 1473;
  Best Local Similarity  63.9%;  Pred. No. 1.7e-48;
  Matches  371;  Conservative    0;  Mismatches  201;  Indels    9;  Gaps    2;

Qy        400 TCTGGCAGTGGTTCCACAACTCGTTATTGGGATTGTTGTAAAGCTTCTTGCAGCTGGCCT 459
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Qy        577 CAACCTTGGGCTGTCAATGATGAGCTCGCTTACGGTTTCGCTGCTGCCTCTATTGCTGGC 636
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